

Letters

Serial Number: 09/242,657B

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☒ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

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FEB 14 2001  
STIC CENTER 1600 1300

#15

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/242,657B

DATE: 02/06/2001  
TIME: 14:59:28

Input Set : A:\Sequence Listing (55411.2).txt  
Output Set: N:\CRF3\02062001\I242657B.raw

1636  
#14  
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FEB 14 2001  
TECH CENTER 1800/2900

537 (D) OTHER INFORMATION:/standard\_name=  
538 "Constitutional promoter"  
539 /label= Cp15  
541 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
E--> 543 CATTACNTAG TTATTCTTG ACAGAATTAC GATTGCTGG TATAATATAT  
544 CAGTACTGTT 60  
546 (2) INFORMATION FOR SEQ ID NO: 12:  
548 (i) SEQUENCE CHARACTERISTICS:  
549 (A) LENGTH: 58 base pairs  
550 (B) TYPE: nucleic acid  
551 (C) STRANDEDNESS: double  
552 (D) TOPOLOGY: linear  
554 (ii) MOLECULE TYPE: DNA (genomic)  
556 (iii) HYPOTHETICAL: YES  
558 (iv) ANTI-SENSE: NO  
560 (vi) ORIGINAL SOURCE:  
561 (A) ORGANISM: Lactococcus lactis  
563 (ix) FEATURE:  
564 (A) NAME/KEY: promoter  
565 (B) LOCATION:4..58  
566 (D) OTHER INFORMATION:/standard\_name=  
567 "Constitutional promoter"  
568 /label= Cp16  
570 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
E--> 572 CATTGTGTAG TTTATTCTTG ACAGCTATGA GTCAATTTGG TATAATAACA  
573 GTACTCAG 58  
575 (2) INFORMATION FOR SEQ ID NO: 13:  
577 (i) SEQUENCE CHARACTERISTICS:  
578 (A) LENGTH: 59 base pairs  
579 (B) TYPE: nucleic acid  
580 (C) STRANDEDNESS: double  
581 (D) TOPOLOGY: linear  
583 (ii) MOLECULE TYPE: DNA (genomic)  
585 (iii) HYPOTHETICAL: YES  
587 (iv) ANTI-SENSE: NO  
589 (vi) ORIGINAL SOURCE:  
590 (A) ORGANISM: Lactococcus lactis  
592 (ix) FEATURE:  
593 (A) NAME/KEY: promoter  
594 (B) LOCATION:4..59  
595 (D) OTHER INFORMATION:/standard\_name=  
596 "Constitutional promoter"  
597 /label= Cp17  
599 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
E--> 601 CATTCTGGAG TTTATTCTTG ACCGCTCAGT ATGCAGTGGT ATAATAGTAC  
602 AGTACTGTT 59  
604 (2) INFORMATION FOR SEQ ID NO: 14:  
606 (i) SEQUENCE CHARACTERISTICS:  
607 (A) LENGTH: 58 base pairs

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608      (B) TYPE: nucleic acid
609      (C) STRANDEDNESS: double
610      (D) TOPOLOGY: linear
612      (ii) MOLECULE TYPE: DNA (genomic)
614      (iii) HYPOTHETICAL: YES
616      (iv) ANTI-SENSE: NO
618      (vi) ORIGINAL SOURCE:
619          (A) ORGANISM: Lactococcus lactis
621      (ix) FEATURE:
622          (A) NAME/KEY: promoter
623          (B) LOCATION:4..58
624          (D) OTHER INFORMATION:/standard_name=
625 "Constitutional promoter"
626 /label= Cp18
628      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
E--> 630 CATTTGCAG TTTATTCTTG ACATTGTGTG CTTCGGGTGT ATAATACTAA
631 GTACTGTT 58
633 (2) INFORMATION FOR SEQ ID NO: 15:
635      (i) SEQUENCE CHARACTERISTICS:
636          (A) LENGTH: 58 base pairs
637          (B) TYPE: nucleic acid
638          (C) STRANDEDNESS: double
639          (D) TOPOLOGY: linear
641      (ii) MOLECULE TYPE: DNA (genomic)
643      (iii) HYPOTHETICAL: YES
645      (iv) ANTI-SENSE: NO
647      (vi) ORIGINAL SOURCE:
648          (A) ORGANISM: Lactococcus lactis
650      (ix) FEATURE:
651          (A) NAME/KEY: promoter
652          (B) LOCATION:4..58
653          (D) OTHER INFORMATION:/standard_name=
654 "Constitutional promoter"
655 /label= Cp19
657      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
E--> 659 CATCGCTTAG TTTTCTTGA CAGGAGGGAT CCGGGTTGAT ATAATAGTTA
660 GTACTGTT 58
662 (2) INFORMATION FOR SEQ ID NO: 16:
664      (i) SEQUENCE CHARACTERISTICS:
665          (A) LENGTH: 60 base pairs
666          (B) TYPE: nucleic acid
667          (C) STRANDEDNESS: double
668          (D) TOPOLOGY: linear
670      (ii) MOLECULE TYPE: DNA (genomic)
672      (iii) HYPOTHETICAL: YES
674      (iv) ANTI-SENSE: NO
676      (vi) ORIGINAL SOURCE:
677          (A) ORGANISM: Lactococcus lactis
679      (ix) FEATURE:

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*same*

*same*

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751      (i) SEQUENCE CHARACTERISTICS:
752          (A) LENGTH: 60 base pairs
753          (B) TYPE: nucleic acid
754          (C) STRANDEDNESS: double
755          (D) TOPOLOGY: linear
757      (ii) MOLECULE TYPE: DNA (genomic)
759      (iii) HYPOTHETICAL: YES
761      (iv) ANTI-SENSE: NO
763      (vi) ORIGINAL SOURCE:
764          (A) ORGANISM: Lactococcus lactis
766      (ix) FEATURE:
767          (A) NAME/KEY: promoter
768          (B) LOCATION:4..60
769          (D) OTHER INFORMATION:/standard_name=
770 "Constitutional promoter"
771 /label= Cp23
772      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
E--> 773 CATGTAGGAG TTTATTCTTG ACAGATTAGT TAGGGGGTGG TATAATATCT
774 CAGTACTGTT 60
776 (2) INFORMATION FOR SEQ ID NO: 20:
778      (i) SEQUENCE CHARACTERISTICS:
779          (A) LENGTH: 60 base pairs
780          (B) TYPE: nucleic acid
781          (C) STRANDEDNESS: double
782          (D) TOPOLOGY: linear
784      (ii) MOLECULE TYPE: DNA (genomic)
786      (iii) HYPOTHETICAL: YES
788      (iv) ANTI-SENSE: NO
790      (vi) ORIGINAL SOURCE:
791          (A) ORGANISM: Lactococcus lactis
793      (ix) FEATURE:
794          (A) NAME/KEY: promoter
795          (B) LOCATION:4..60
796          (D) OTHER INFORMATION:/standard_name=
797 "Constitutional promoter"
798 /label= Cp24
800      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
E--> 802 CATGGGTAAG TTTATTCTTC ACACATCTCG GGCCCGATGG TATAATAAGT
803 GACTACTGTT 60
805 (2) INFORMATION FOR SEQ ID NO: 21:
807      (i) SEQUENCE CHARACTERISTICS:
808          (A) LENGTH: 59 base pairs
809          (B) TYPE: nucleic acid
810          (C) STRANDEDNESS: double
811          (D) TOPOLOGY: linear
813      (ii) MOLECULE TYPE: DNA (genomic)
815      (iii) HYPOTHETICAL: YES
817      (iv) ANTI-SENSE: NO
819      (vi) ORIGINAL SOURCE:

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*same*

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820      (A) ORGANISM: Lactococcus lactis
822      (ix) FEATURE:
823      (A) NAME/KEY: promoter
824      (B) LOCATION:3..59
825      (D) OTHER INFORMATION:/standard_name=
826 "Constitutional promoter"
827 /label= Cp25
828      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
E--> 830 CTTTGGCAGT TTATTCTTGA CATGTAGTGA GGGGGCTGGT ATAATCACAT
831 AGTACTGTT 59
1484 (2) INFORMATION FOR SEQ ID NO: 43:
1486      (i) SEQUENCE CHARACTERISTICS:
1487      (A) LENGTH: 177 base pairs
1488      (B) TYPE: nucleic acid
1489      (C) STRANDEDNESS: double
1490      (D) TOPOLOGY: linear
1492      (ii) MOLECULE TYPE: DNA (genomic)
1494      (iii) HYPOTHETICAL: YES
1496      (iv) ANTI-SENSE: NO
1498      (vi) ORIGINAL SOURCE:
1499      (A) ORGANISM: Saccharomyces cerevisiae
1501      (ix) FEATURE:
1502      (A) NAME/KEY: promoter
1503      (B) LOCATION:8..177
1504      (C) IDENTIFICATION METHOD: experimental
1505      (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1506 /standard_name= "Yeast promoter"
1507 /label= Yp102
1508      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
E--> 1510 GAATTCGTGA CTCAAACGGG TGGTCGACGG GTGGTTCCAA TTAATTGGCG
1511 TCCCTCTTAT      60
E--> 1513 AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT
1514 GCAAGTGACT      120
E--> 1516 GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC
W--> 1517 177
1520 (2) INFORMATION FOR SEQ ID NO: 44:
1522      (i) SEQUENCE CHARACTERISTICS:
1523      (A) LENGTH: 182 base pairs
1524      (B) TYPE: nucleic acid
1525      (C) STRANDEDNESS: double
1526      (D) TOPOLOGY: linear
1528      (ii) MOLECULE TYPE: DNA (genomic)
1530      (iii) HYPOTHETICAL: YES
1532      (iv) ANTI-SENSE: NO
1534      (vi) ORIGINAL SOURCE:
1535      (A) ORGANISM: Saccharomyces cerevisiae
1537      (ix) FEATURE:
1538      (A) NAME/KEY: promoter
1539      (B) LOCATION:8..181

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1540          (C) IDENTIFICATION METHOD: experimental
1541          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1542 /standard_name= "Yeast promoter"
1543 /label= Yp112
1545          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
E--> 1547 GAATTCGTGA CTCACGGCAT CTGATGGTTG ACCATAGTCA GGAACATTGT
1548 GCTGGAGTTC          60
E--> 1550 CTGAGGAAT GAGTTATAAA ATGGGAGGTT GCGGCTAATG CCAGGCAGGA
1551 GAGGAACCCCT          120
E--> 1553 CTTAAGTGCA AGTGACTGCA AACATTTTTT TCGTTTGTG AATCGCTACC
1554 AATCATGGAT          180
E--> 1556 CC
W--> 1557 182
1560 (2) INFORMATION FOR SEQ ID NO: 45:
1562 (i) SEQUENCE CHARACTERISTICS:
1563 (A) LENGTH: 191 base pairs
1564 (B) TYPE: nucleic acid
1565 (C) STRANDEDNESS: double
1566 (D) TOPOLOGY: linear
1568 (ii) MOLECULE TYPE: DNA (genomic)
1570 (iii) HYPOTHETICAL: YES
1572 (iv) ANTI-SENSE: NO
1574 (vi) ORIGINAL SOURCE:
1575 (A) ORGANISM: Saccharomyces cerevisiae
1577 (ix) FEATURE:
1578 (A) NAME/KEY: promoter
1579 (B) LOCATION:8..181
1580 (C) IDENTIFICATION METHOD: experimental
1581 (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1582 /standard_name= "Yeast promoter"
1583 /label= Yp13
1585          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
E--> 1587 GAATTCGTGA CTCACTAGGC AGGTCACGTT GGCTCTTCGC GGCGCAGGTT
1588 CGTATGCCGC          60
E--> 1590 GCCGCCAGGG GCTTTATAAA GGTCGTCCTG GGTACAGTTG GGATGGCTCC
1591 ACGTTTCGGC          120
E--> 1593 TCTTAAGTGC AAGTGACTGC GAACATTTCG TTTGTTAGAA TAATTCAAGA
1594 ATCGCTACCA          180
E--> 1596 ATCATGGATC C
W--> 1597 191
1600 (2) INFORMATION FOR SEQ ID NO: 46:
1602 (i) SEQUENCE CHARACTERISTICS:
1603 (A) LENGTH: 167 base pairs
1604 (B) TYPE: nucleic acid
1605 (C) STRANDEDNESS: double
1606 (D) TOPOLOGY: linear
1608 (ii) MOLECULE TYPE: DNA (genomic)
1610 (iii) HYPOTHETICAL: YES
1612 (iv) ANTI-SENSE: NO

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*same*

RAW SEQUENCE LISTING                      DATE: 02/06/2001  
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 Output Set: N:\CRF3\02062001\I242657B.raw

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1614      (vi) ORIGINAL SOURCE:
1615          (A) ORGANISM: Saccharomyces cerevisiae
1617      (ix) FEATURE:
1618          (A) NAME/KEY: promoter
1619          (B) LOCATION:8..167
1620          (C) IDENTIFICATION METHOD: experimental
1621          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1622 /standard_name= "Yeast promoter"
1623 /label= Yp15
1625      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
E--> 1627 GAATTCGTGA CTCAGGGCCG TACTAAGTAG CTTTCGTATG CTATGCGGGG
1628 TTTTATAAAT      60
E--> 1630 CTTTGGGCCA TGGTCTTGCT GGAAAACACC TCTCTTAAGT GCAAGTGACT
1631 GCGAACATTT      120
E--> 1633 TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA TGGATCC
W--> 1634 167
1637 (2) INFORMATION FOR SEQ ID NO: 47:
1639      (i) SEQUENCE CHARACTERISTICS:
1640          (A) LENGTH: 191 base pairs
1641          (B) TYPE: nucleic acid
1642          (C) STRANDEDNESS: double
1643          (D) TOPOLOGY: linear
1645      (ii) MOLECULE TYPE: DNA (genomic)
1647      (iii) HYPOTHETICAL: YES
1649      (iv) ANTI-SENSE: NO
1651      (vi) ORIGINAL SOURCE:
1652          (A) ORGANISM: Saccharomyces cerevisiae
1654      (ix) FEATURE:
1655          (A) NAME/KEY: promoter
1656          (B) LOCATION:8..191
1657          (C) IDENTIFICATION METHOD: experimental
1658          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1659 /standard_name= "Yeast promoter"
1660 /label= Yp154
1662      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
E--> 1664 GAATTCGTGA CTCACCGCTC GGGTGCAGGG CCAAGGCGGC GGAATGTGCG
1665 GGGCGTTCTA      60
E--> 1667 GCGCAATCGG GGTATAAATT TATAAGGAGG CTGCGGGTGC TAGTTGTCT
1668 AGTTTGACTC      120
E--> 1670 TTAAGTGCAA GTGACTGCCA ACATTTTTCG TTTGTTAGAA TAATTCAAGA
1671 ATCGCTACCA      180
E--> 1673 ATCATGGATC C
W--> 1674 191
1677 (2) INFORMATION FOR SEQ ID NO: 48:
1679      (i) SEQUENCE CHARACTERISTICS:
1680          (A) LENGTH: 195 base pairs
1681          (B) TYPE: nucleic acid
1682          (C) STRANDEDNESS: double
1683          (D) TOPOLOGY: linear

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1685      (ii) MOLECULE TYPE: DNA (genomic)
1687      (iii) HYPOTHETICAL: YES
1689      (iv) ANTI-SENSE: NO
1691      (vi) ORIGINAL SOURCE:
1692          (A) ORGANISM: Saccharomyces cerevisiae
1694      (ix) FEATURE:
1695          (A) NAME/KEY: promoter
1696          (B) LOCATION:8..190
1697          (C) IDENTIFICATION METHOD: experimental
1698          (D) OTHER INFORMATION:/evidence= EXPERIMENTAL
1699 /standard_name= "Yeast promoter"
1700 /label= Yp18
1702      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
E--> 1704 GAATTCGTGA CTCAGGATTA GCTATGCCGG TTGGGATAAG CGAACAACTG
1705 GAGGTGAGAA      60
E--> 1707 GCTTTTTGTC AGAATATAAA CCCGTTAGTC AGGGTTTGGT GGGATAGGGG
1708 GTACTGTACC      120
E--> 1710 TCTTAAGTGC AAGTGACTGC GAACATTTT TTCGTTTGTT AGAATAATTC
1711 AAGAATCGCT      180
E--> 1713 ACCAATCATG GATCC
W--> 1714 195

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## VERIFICATION SUMMARY

DATE: 02/06/2001

PATENT APPLICATION: US/09/242,657B

TIME: 14:59:29

Input Set : A:\Sequence Listing (55411.2).txt

Output Set: N:\CRF3\02062001\I242657B.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:39 M:220 C: Keyword misspelled or invalid format, [(C) REFERENCE/DOCKET NUMBER:]  
L:124 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:1  
L:212 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:2  
M:254 Repeated in SeqNo=2  
L:216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:303 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:3  
M:254 Repeated in SeqNo=3  
L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:372 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:5  
L:400 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:6  
L:428 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:7  
L:456 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:8  
L:485 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:9  
L:514 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:10  
L:543 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:11  
L:572 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:12  
L:601 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:13  
L:630 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:14  
L:659 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:15  
L:688 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:16  
L:717 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:17  
L:746 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:18  
L:773 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:19  
L:802 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:20  
L:830 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:21  
L:859 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:22  
L:890 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:23  
L:921 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:24  
L:952 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:25  
L:983 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:26  
L:1014 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:27  
L:1045 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:28  
L:1076 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:29  
L:1108 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:30  
L:1139 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:31  
L:1170 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:32  
L:1201 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:33  
L:1232 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:34  
L:1263 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:35  
L:1294 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:36  
L:1325 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:37  
L:1356 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:38  
L:1387 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:39  
L:1418 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:40  
L:1449 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:41  
L:1480 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:42

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Input Set : A:\Sequence Listing (55411.2).txt

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L:1510 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:43  
M:254 Repeated in SeqNo=43  
L:1517 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43  
L:1547 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:44  
M:254 Repeated in SeqNo=44  
L:1557 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44  
L:1587 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:45  
M:254 Repeated in SeqNo=45  
L:1597 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45  
L:1627 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:46  
L:1634 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46  
L:1674 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:47  
L:1714 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:48  
L:1791 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50  
L:1831 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:51  
L:1868 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52  
L:1908 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53  
L:1948 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54  
L:1988 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:55  
L:2028 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:56  
L:2068 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:57  
L:2105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:58